

IN THE CLAIMS:

Please amend claims 1-6, 8, 10-12 and 14-15 as follows:

1. (Currently Amended) A method for displaying a dendrogram comprising the steps of:
clustering a plurality of biopolymers based on a set of gene expression data obtained by experiments under different conditions on the plurality of biopolymers, and displaying clustering results thereof in a form of a dendrogram in a display window;
selecting a subtree in the dendrogram in the display window; [[and]]
displaying the selected subtree [[on]]in a separate display window; [[thereby]]
grouping biopolymers in the selected subtree in the separate display window into at least one function group sharing a common one of functional characteristics including enzymatic, metabolic, transporting, and cell cycle functions; and
displaying said function group of biopolymers in the separate display window.
2. (Currently Amended) A method for displaying a dendrogram according to claim 1, further comprising the steps of:
~~designating a different clustering method for said grouping step biopolymers included in the subtree displayed on the separate window; and~~
~~secondarily clustering the biopolymers included in the subtree according to the designated clustering method, and~~
~~displaying the secondarily clustering results thereof in a form of a dendrogram.~~
3. (Currently Amended) A method for displaying a dendrogram comprising the steps of:
clustering a plurality of biopolymers based on a set of gene expression data obtained by experiments under different conditions on the plurality of biopolymers, and displaying clustering results thereof in a form of a dendrogram in a display window;
selecting a subtree in the dendrogram in the display window; [[and]]
replacing the selected subtree with an icon in the dendrogram thereby simplifying a presentation in the display window; [[thereby]]

grouping biopolymers ~~in the selected subtree in the simplified presentation in the display window~~ into at least one function group sharing a common one of functional characteristics including enzymatic, metabolic, transporting, and cell cycle functions; and

displaying said function group of biopolymers in the simplified presentation in the display window.

4. (Currently Amended) A method for displaying a dendrogram according to claim 3, further comprising a step of restoring ~~the icon back to the selected subtree back from the replacing icon~~ in the dendrogram in the display window.
5. (Currently Amended) A method for displaying a dendrogram comprising the steps of:
 - clustering a plurality of biopolymers based on a set of gene expression data obtained by experiments under different conditions on the plurality of biopolymers, and displaying clustering results thereof in a form of a dendrogram in a display window;
 - selecting a subtree in the dendrogram in the display window;
 - selecting keywords from a keyword dictionary file; and
 - counting biopolymers in the subtree whose biopolymer information contains at least one of the selected predetermined keywords in the selected subtree and displaying each of the selected predetermined keywords with a corresponding count of the biopolymers whose biopolymer information contains at least one of the selected predetermined keywords; [[thereby]]
 - grouping biopolymers in the selected subtree into at least one function group sharing a common one of functional characteristics including enzymatic, metabolic, transporting, and cell cycle functions;
 - displaying said function group of biopolymers in the display window; and
 - displaying the selected keywords and said count in a separated display window on top of the display window displaying said function group of biopolymers therein thereby confirming relative biopolymers are assembled in the selected subtree, wherein said biopolymer information includes a unique nucleotide sequence identifier and a description of a corresponding nucleotide sequence, said description includes a source organism, a gene name/protein name, or a function.

6. (Currently Amended) A method for displaying a dendrogram comprising the steps of:
clustering a plurality of biopolymers based on a set of gene expression data obtained by experiments under different conditions on the plurality of biopolymers, and displaying clustering results thereof in a form of a dendrogram in a display window;
selecting a subtree in the dendrogram in the display window;
designating at least one keyword [[for]] from a keyword dictionary file;
searching in the selected subtree for biopolymers whose biopolymer information contains the designated keyword; and
~~displaying the selected subtree and highlighting in the display window a location of each of the biopolymers in the selected subtree whose biopolymer information contains the designated keyword; [[thereby]]~~
grouping biopolymers in the selected subtree into at least one function group sharing a common one of functional characteristics including enzymatic, metabolic, transporting, and cell cycle functions;
~~displaying the highlighted keywords together with said function group of biopolymers in the display window thereby confirming relative biopolymers are assembled in the selected subtree,~~
wherein said biopolymer information includes a unique nucleotide sequence identifier and a description of a corresponding nucleotide sequence, said description includes a source organism, a gene name/protein name, or a function.
7. (Original) A method for displaying a dendrogram according to any one of claims 1 to 6, wherein the biopolymers are cDNAs, RNAs, DNA fragments or genes.
8. (Currently Amended) A system for displaying a dendrogram comprising:
a clustering processor for clustering a plurality of biopolymers based on a set of gene expression data obtained by experiments under different conditions on the plurality of biopolymers, and analyzing and displaying clustering results thereof in a form of a dendrogram in a display window;
a display system for displaying the dendrogram, [[and]] for displaying on a separate window a subtree selected by a user in the display window thereby grouping

biopolymers in the selected subtree in the separate display window into at least one function group sharing a common one of functional characteristics including enzymatic, metabolic, transporting, and cell cycle functions, and for displaying said function group of biopolymers in the separate display window; and

a keyword dictionary file for storing keywords of biopolymer information associated with each of the plurality types of biopolymers, said biopolymer information including a unique nucleotide sequence identifier and a description of a corresponding nucleotide sequence, said description includes a source organism, a gene name/protein name, or a function.

9. (Previously Presented) A system for displaying a dendrogram according to claim 8, further comprising input means for selecting the subtree by the user.
10. (Currently Amended) A system for displaying a dendrogram according to claim 8, further comprising means for designating a different clustering method for said grouping biopolymers in the selected subtree displayed on the separate window to secondarily cluster biopolymers included in the subtree according to the designated clustering method, wherein the display system displays and displaying secondarily clustering results thereof clustered biopolymers in the selected subtree in a form of a dendrogram.
11. (Currently Amended) A system for displaying a dendrogram according to any one of claims 8 to 10, further comprising means for replacing the selected subtree with an icon, and means for restoring the icon back to the selected subtree back from the replacing icon in the dendrogram in the display window.
12. (Currently Amended) A system for displaying a dendrogram according to any one of claims 8 to 10, further comprising one of means for retrieving keywords from the keyword dictionary file, means for counting biopolymers in the subtree whose biopolymer information contains at least one of the retrieved predetermined keywords retrieved from the keyword dictionary file and displaying, wherein the display system displays each of the retrieved predetermined keywords with a corresponding count of the biopolymers whose biopolymer information contains at least one of the retrieved

predetermined keywords, and highlights[[ing]] a location of each of the biopolymers in the selected subtree whose biopolymer information contains at least one of the retrieved predetermined keywords.

13. (Previously Presented) A system for displaying a dendrogram according to any one of claims 8 to 10, wherein the biopolymers are cDNAs, RNAs, DNA fragments or genes.
14. (Currently Amended) A method for displaying a dendrogram according to claim 5, wherein the counting step involves counting biopolymers in the selected subtree whose biopolymer information contains synonyms of said one of the selected predetermined keywords.
15. (Currently Amended) A system for displaying a dendrogram according to claim 12, wherein the means for counting ~~and displaying~~ counts biopolymers in the selected subtree whose biopolymer information contains synonyms of each of the retrieved predetermined keywords.